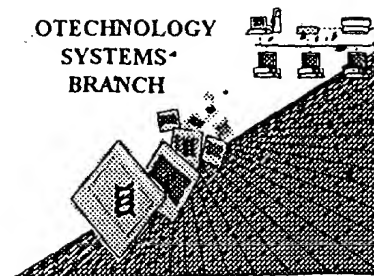# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09 936 845_

Source: _PCT 09_

Date Processed by STIC: _10 03 01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

```
                RAW SEQUENCE LISTING              DATE: 10/03/2001
                PATENT APPLICATION:  US/09/936,845    TIME: 10:29:43

                Input Set : A:\NAPIER PCT-GB00-01035 sequence listing.txt
                Output Set: N:\CRF3\10032001\I936845.raw

     3 <110> APPLICANT: Napier, Johnathan A.
     5 <120> TITLE OF INVENTION: Polyunsaturated Fatty Acid (PUFA) Elongase from
Caenorhabditis elegans
     7 <130> FILE REFERENCE: 76/7
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/936,845
C--> 10 <141> CURRENT FILING DATE: 2001-09-18
    12 <160> NUMBER OF SEQ ID NOS: 22
    14 <170> SOFTWARE: PatentIn Ver. 2.1
```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

Handwritten note: Must enumerate unknown proteins in 221, 222 and 223. Specifically, you must specify a "variant", location and values for Xaa

```
   728 <210> SEQ ID NO: 22
   729 <211> LENGTH: 269
   730 <212> TYPE: PRT
   731 <213> ORGANISM: C. elegans
   733 <400> SEQUENCE: 22
   734 Met Ser Ala Glu Val Ser Glu Arg Phe Lys Val Trp Thr Gly Asn Asn
   735  1               5                  10                  15
   737 Glu Thr Ile Ile Tyr Ser Pro Phe Glu Tyr Asp Ser Thr Leu Leu Ile
   738              20                  25                  30
   740 Glu Ser Cys Arg Cys Thr Tyr Gln Leu Leu Ile Leu Leu Arg Gln Ile
   741          35                  40                  45
E--> 743 Tyr Tyr Arg Asp Ile Trp Ser His Gly Asn Leu Lys Ala Cys Asp Xaa
   744      50                  55                  60
   746 Leu Leu Leu Ala Trp Asn Gly Phe Leu Ala Val Phe Ser Ile Met Gly
   747 65                  70                  75                  80
E--> 749 Thr Trp Arg Phe Gly Ile Glu Phe Tyr Asp Ala Val Phe Arg Xaa Gly
   750              85                  90                  95
E--> 752 Phe Ile Xaa Ser Ile Cys Leu Ala Val Asn Pro Arg Ser Pro Ser Ala
   753          100                 105                 110
   755 Phe Trp Ala Cys Met Phe Ala Leu Ser Lys Ile Ala Glu Phe Gly Asp
   756          115                 120                 125
   758 Thr Met Phe Leu Val Leu Arg Lys Arg Pro Val Ile Phe Leu His Trp
   759      130                 135                 140
   761 Tyr His His Ala Val Val Leu Ile Leu Ser Trp His Ala Ala Ile Glu
   762 145                 150                 155                 160
   764 Leu Thr Ala Pro Gly Arg Trp Phe Ile Phe Met Asn Tyr Leu Val His
   765              165                 170                 175
E--> 767 Ser Ile Met Tyr Thr Tyr Tyr Ala Ile Thr Ser Ile Gly Tyr Arg Xaa
   768          180                 185                 190
   770 Pro Lys Ile Val Ser Met Thr Val Thr Phe Leu Gln Thr Leu Gln Met
   771          195                 200                 205
   773 Leu Ile Gly Val Ser Ile Ser Cys Ile Val Leu Tyr Leu Lys Leu Asn
   774      210                 215                 220
   776 Gly Glu Met Cys Gln Gln Ser Tyr Asp Asn Leu Ala Leu Ser Phe Gly
   777 225                 230                 235                 240
   779 Ile Tyr Ala Ser Phe Leu Val Leu Ser Ser Phe Phe Asn Asn Ala Tyr
```

RAW SEQUENCE LISTING   DATE: 10/03/2001
PATENT APPLICATION: US/09/936,845   TIME: 10:29:43

Input Set : **A:\NAPIER PCT-GB00-01035 sequence listing.txt**
Output Set: **N:\CRF3\10032001\I936845.raw**

```
780                245                250                          255
782 Leu Val Lys Lys Asp Lys Lys Pro Asp Val Lys Lys Asp
783                260                265
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/936,845**
DATE: 10/03/2001
TIME: 10:29:44

Input Set : **A:\NAPIER PCT-GB00-01035 sequence listing.txt**
Output Set: **N:\CRF3\10032001\I936845.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:743 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
M:340 Repeated in SeqNo=22

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09 936 845

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length.

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
(OLD RULES)

Sequence(s)____missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)　　　SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES)

Sequence(s)____missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9 ✓ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s)____missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)　(Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001